LISTING OF CLAIMS

This Listing of Claims will replace all prior versions of claims in the application.

Claim 1-31 (Cancelled)

Claim 32 (Previously presented) A method for analyzing a nucleic acid sample comprising:

    (a)   obtaining a nucleic acid sample by cutting and linearizing a strand of nucleic acid;

    (b)   preparing a surface;

    (c)   tethering the linearized nucleic acid sample to the surface;

    (d)   tagging two or more sequence specific sites of the tethered nucleic acid sample with a sequence specific tag;

    (e)   drying the nucleic acid sample;

    (f)   scanning the nucleic acid sample with a scanning probe microscope; and

    (g)   analyzing the scan to determine the distance between the tagged nucleic acid sites.

Claim 33 (Previously presented) The method of claim 32 wherein preparing the surface further comprises modifying the surface with an alkanethiolate.

Claim 34 (Previously presented) The method of claim 32 wherein tethering the linearized nucleic acid sample to the surface further comprises modifying one or both ends of the nucleic acid sample with a reactive group that will react with the prepared surface.

Claim 35 (Previously presented) The method of claim 32 wherein scanning the nucleic acid sample further comprises bleeding a low moisture inert gas over the tethered nucleic acid sample.

Claim 36 (Previously presented) The method of claim 32 wherein analyzing the scan further comprises forming bar code readouts wherein the bars represent a tagged nucleic acid sample and the distance between the bars represents the distance between the tagged sequence specific sites.

Claim 37 (Previously presented) The method of claim ~~12~~ 32 further comprising tethering the

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nucleic acid sample to a deposition surface.

Claim 38 (Previously presented) The method of claim 37 wherein the deposition surface is on a dipstick.

Claim 39 (Currently amended) The method of claim ~~28~~ 38 wherein the deposition surface on the dipstick has specific areas for tethering different types of nucleic acid sequences.

Claim 40 (Cancelled)

Claim 41 (New) A method for analyzing a nucleic acid sample comprising:
  (a)   obtaining a nucleic acid sample by cutting and linearizing a strand of nucleic acid;
  (b)   preparing a surface;
  (c)   tethering the linearized nucleic acid sample to the surface;
  (d)   tagging two or more sequence specific sites of the tethered nucleic acid sample with a sequence specific tag;
  (e)   scanning the nucleic acid sample with a scanning probe microscope; and
  (f)   analyzing the scan to determine the distance between the tagged nucleic acid sites.